

AMENDMENTS TO THE CLAIMS:

1-10. (Canceled)

11. (Presently Amended) The method of claim 19, characterised in that the **universal**-primers are **selected from the group consisting of:**

5'TCCGGCATGTGCAAGGCCGG3' (SEQ ID NO: 1)**[[,]] and**

5'CTCCATGTCTCCAGTTGG3' (SEQ ID NO: 2)**[[,]]**

5'ACGAACTGGGACGACATGGAGAAGATCTGGC3' (SEQ ID NO: 3),

5'TAGATGGCNGGGGTGTTAAAGGTCTCAAAC3' (SEQ ID NO: 4),

5'TGGCCTGAGGCCCTCTTCAGCCTTCCTTC3' (SEQ ID NO: 5),

5'GGGTACATGGTGGTGGCGGCAGACAGCACNGTGTGGC3' (SEQ ID NO: 6),

5'GCCAAGACNGTGCTGTCTGGCGGCACCACCATGTACCC3' (SEQ ID NO: 7) and

5'TCGTACTCCTGCTTGCTGATCCACATCTG3' (SEQ ID NO: 8).

12. (Previously Canceled)

13. (Presently Amended) The method of claim 16, characterised in that the sample is taken from horse, goat, rabbit, dog, cat, chimpanzee, human **[[and/]]** or brown bear tissue.

14 -15. (Previously Canceled)

16. (Presently Amended) A method for genetic identification of biological species using a sample of biological material derived from a single species or from a heterogeneous mixture of species and/or subspecies, characterised in that it comprises:

- (a) DNA extraction from the sample;
- (b) amplification of a one or more-region[[s]] of the DNA of the sample, said ~~one or more~~-region[[s]] ~~selected from the group consisting of a region~~-corresponding to the region between positions 1130 and 1473 of the human cytoplasmic beta-actin gene, ~~a region corresponding to the region between positions 1452 and 2063 of the human cytoplasmic beta-actin gene, a region corresponding to the region between positions 2438 and 2680 of the human cytoplasmic beta-actin gene, and a region corresponding to the region between positions 2642 and 2960 of the human cytoplasmic beta-actin gene,~~ said position numbers being relative to SEQ ID NO:9 ~~which comprises the full DNA sequence of the human locus HUMACCYBB Accession number M10277, verison M10277.1, GI:477967, wherein said region is~~ amplified using DNA oligonucleotide primers that hybridize with

conserved sequences between positions 1130 and 1473 of SEQ ID

NO:9;

(c) analysis of the **one-or-more-amplified** region[[s]] to determine the size in base-pairs and/or the precise DNA sequence thereof; and

(d) taxonomic identification of the biological species or subspecies from which the sample was derived by comparison of the size and/or DNA sequence ~~characteristics~~ of said one or more amplified region[[s]] with a database containing pre-established sizes and/or DNA sequences ~~characteristics~~ of the corresponding region[[s]] of the cytoplasmic beta-actin gene of a plurality of species and/or subspecies.

17. (Presently Amended) The method of claim 16, characterised in that in the amplification step gene segments of **evolutionary-evolutionarily** divergent regions of the cytoplasmic beta-actin gene are amplified using DNA oligonucleotide primers **corresponding to ranges of nucleotide positions in SEQ ID NO:9 having greater than 98% sequence identity among the species and sub-species present in the database having evolutionary DNA sequence conservation greater than 98% between species and subspecies.**

18. (Presently Amended) The method of claim 16, characterised in that in the amplification step the segments to be amplified comprise the whole intronic DNA sequence and at least a portion of the flanking exonic sequences relative to SEQ ID NO:9, for each of the B, C, D and E introns as annotated in the GenBank Record of the human locus HUMAGCYBB Accession number M10277, verison M10277.1, GI:177967.

19. (Presently Amended) The method of claim 16, characterised in that in the amplification step primers are used it uses a composition of universal primers that hybridise-hybridize with one or more sequences within regions of the cytoplasmic beta-actin gene selected from the group consisting of the regions between positions 1130 to 1191 and 1453 to 1473 of the cytoplasmic beta-actin gene[[.]] the region between positions 1452 and 2063 of the cytoplasmic beta-actin gene, the region between positions 2438 and 2680 of the cytoplasmic beta-actin gene, and the region between positions 2642 and 2960 of the cytoplasmic beta-actin gene, said position numbers being relative to SEQ ID NO:9 which comprises the full DNA sequence of the human locus HUMAGCYBB Accession number M10277, verison M10277.1, GI:177967.